

# Norihiro Kato

## List of Publications by Citations

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85  
papers

6,440  
citations

38  
h-index

80  
g-index

89  
ext. papers

8,308  
ext. citations

11.3  
avg, IF

4.44  
L-index

| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 85 | Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , <b>2018</b> , 50, 524-537  | 36.3 | 536       |
| 84 | Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , <b>2017</b> , 541, 81-86   | 50.4 | 511       |
| 83 | Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , <b>2011</b> , 44, 67-72  | 36.3 | 475       |
| 82 | Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. <i>Nature Genetics</i> , <b>2011</b> , 43, 531-8  | 36.3 | 442       |
| 81 | Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , <b>2011</b> , 43, 984-9  | 36.3 | 406       |
| 80 | Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 403-415  | 36.3 | 313       |
| 79 | Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , <b>2012</b> , 44, 307-11   | 36.3 | 301       |
| 78 | Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , <b>2015</b> , 47, 1282-1293                                     | 36.3 | 223       |
| 77 | Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , <b>2017</b> , 14, e1002383           | 11.6 | 223       |
| 76 | Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , <b>2012</b> , 44, 904-9  | 36.3 | 201       |
| 75 | Confirmation of multiple risk Loci and genetic impacts by a genome-wide association study of type 2 diabetes in the Japanese population. <i>Diabetes</i> , <b>2009</b> , 58, 1690-9  | 0.9  | 196       |
| 74 | Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. <i>Nature Genetics</i> , <b>2012</b> , 44, 302-6   | 36.3 | 192       |
| 73 | Blood pressure and hypertension are associated with 7 loci in the Japanese population. <i>Circulation</i> , <b>2010</b> , 121, 2302-9  | 16.7 | 147       |
| 72 | Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 545-54 | 11   | 145       |
| 71 | Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 5492-504   | 5.6  | 141       |
| 70 | Genome-wide association study of coronary artery disease in the Japanese. <i>European Journal of Human Genetics</i> , <b>2012</b> , 20, 333-40   | 5.3  | 123       |
| 69 | Confirmation of ALDH2 as a Major locus of drinking behavior and of its variants regulating multiple metabolic phenotypes in a Japanese population. <i>Circulation Journal</i> , <b>2011</b> , 75, 911-8                                | 2.9  | 104       |

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|----|---|------|----|
| 68 | Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 1770-1784 | 5.6  | 90 |
| 67 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , <b>2020</b> , 582, 240-245  | 50.4 | 89 |
| 66 | Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 1791-800  | 5.6  | 71 |
| 65 | Genome-wide association study meta-analysis reveals transethnic replication of mean arterial and pulse pressure loci. <i>Hypertension</i> , <b>2013</b> , 62, 853-9   | 8.5  | 60 |
| 64 | Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , <b>2019</b> , 51, 636-648   | 36.3 | 59 |
| 63 | A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 375-400                          | 11   | 59 |
| 62 | Association of genetic variants for susceptibility to obesity with type 2 diabetes in Japanese individuals. <i>Diabetologia</i> , <b>2011</b> , 54, 1350-9  | 10.3 | 58 |
| 61 | Deletion of CDKAL1 affects mitochondrial ATP generation and first-phase insulin exocytosis. <i>PLoS ONE</i> , <b>2010</b> , 5, e15553   | 3.7  | 57 |
| 60 | Absence of Cd36 mutation in the original spontaneously hypertensive rats with insulin resistance. <i>Nature Genetics</i> , <b>1999</b> , 22, 226-8  | 36.3 | 54 |
| 59 | A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1108-19   | 5.6  | 53 |
| 58 | Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. <i>Circulation Research</i> , <b>2017</b> , 121, 81-88  | 15.7 | 48 |
| 57 | Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , <b>2016</b> , 6, 17958  | 4.9  | 48 |
| 56 | Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 2303-11   | 5.6  | 48 |
| 55 | Insights into the genetic basis of type 2 diabetes. <i>Journal of Diabetes Investigation</i> , <b>2013</b> , 4, 233-44  | 3.9  | 44 |
| 54 | High-density association study and nomination of susceptibility genes for hypertension in the Japanese National Project. <i>Human Molecular Genetics</i> , <b>2008</b> , 17, 617-27   | 5.6  | 44 |
| 53 | Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. <i>Diabetes</i> , <b>2015</b> , 64, 291-8  | 0.9  | 43 |
| 52 | Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , <b>2019</b> , 2, 115   | 6.7  | 42 |
| 51 | Gene-environmental interaction regarding alcohol-metabolizing enzymes in the Japanese general population. <i>Hypertension Research</i> , <b>2009</b> , 32, 207-13   | 4.7  | 42 |

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|----|---|------|----|
| 50 | Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , <b>2019</b> , 10, 376  | 17.4 | 41 |
| 49 | Ethnic differences in genetic predisposition to hypertension. <i>Hypertension Research</i> , <b>2012</b> , 35, 574-81   | 4.7  | 41 |
| 48 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1033-1054   | 3.8  | 39 |
| 47 | Reevaluation of the association of seven candidate genes with blood pressure and hypertension: a replication study and meta-analysis with a larger sample size. <i>Hypertension Research</i> , <b>2012</b> , 35, 825-31 | 4.7  | 38 |
| 46 | Non-alcoholic fatty liver disease in a rural, physically active, low income population in Sri Lanka. <i>BMC Research Notes</i> , <b>2011</b> , 4, 513   | 2.3  | 38 |
| 45 | Association of genetic variants influencing lipid levels with coronary artery disease in Japanese individuals. <i>PLoS ONE</i> , <b>2012</b> , 7, e46385  | 3.7  | 38 |
| 44 | Isolation of a chromosome 1 region affecting blood pressure and vascular disease traits in the stroke-prone rat model. <i>Hypertension</i> , <b>2003</b> , 42, 1191-7   | 8.5  | 36 |
| 43 | Genetic analysis in human hypertension. <i>Hypertension Research</i> , <b>2002</b> , 25, 319-27   | 4.7  | 34 |
| 42 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198166                                | 3.7  | 31 |
| 41 | Identification of quantitative trait loci for serum cholesterol levels in stroke-prone spontaneously hypertensive rats. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2000</b> , 20, 223-9             | 9.4  | 31 |
| 40 | Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , <b>2018</b> , 9, 5052   | 17.4 | 29 |
| 39 | Analysis of KRAP expression and localization, and genes regulated by KRAP in a human colon cancer cell line. <i>Journal of Human Genetics</i> , <b>2007</b> , 52, 978-984   | 4.3  | 24 |
| 38 | Genome-wide searches for blood pressure quantitative trait loci in the stroke-prone spontaneously hypertensive rat of a Japanese colony. <i>Journal of Hypertension</i> , <b>2003</b> , 21, 295-303                     | 1.9  | 24 |
| 37 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , <b>2021</b> ,  | 50.4 | 24 |
| 36 | Deletion of CDKAL1 affects high-fat diet-induced fat accumulation and glucose-stimulated insulin secretion in mice, indicating relevance to diabetes. <i>PLoS ONE</i> , <b>2012</b> , 7, e49055                         | 3.7  | 22 |
| 35 | The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , <b>2017</b> , 12, e0185487   | 3.7  | 21 |
| 34 | The stroke-prone spontaneously hypertensive rat: still a useful model for post-GWAS genetic studies?. <i>Hypertension Research</i> , <b>2012</b> , 35, 477-84   | 4.7  | 21 |
| 33 | Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 2070-2081                                | 5.6  | 20 |

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|----|--|------|----|
| 32 | Genome-wide linkage analysis of type 2 diabetes mellitus reconfirms the susceptibility locus on 11p13-p12 in Japanese. <i>Journal of Human Genetics</i> , <b>2004</b> , 49, 629-634  | 4.3  | 18 |
| 31 | Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. <i>European Journal of Preventive Cardiology</i> , <b>2017</b> , 24, 492-504   | 3.9  | 16 |
| 30 | A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 2615-2633   | 5.6  | 14 |
| 29 | Identification of quantitative trait loci for cardiac hypertrophy in two different strains of the spontaneously hypertensive rat. <i>Hypertension Research</i> , <b>2005</b> , 28, 273-81  | 4.7  | 13 |
| 28 | Identification of a genetic variant at 2q12.1 associated with blood pressure in East Asians by genome-wide scan including gene-environment interactions. <i>BMC Medical Genetics</i> , <b>2014</b> , 15, 65  | 2.1  | 12 |
| 27 | Lysosome biogenesis regulated by the amino-acid transporter SLC15A4 is critical for functional integrity of mast cells. <i>International Immunology</i> , <b>2017</b> , 29, 551-566  | 4.9  | 10 |
| 26 | Systemic evaluation of gene expression changes in major target organs induced by atorvastatin. <i>European Journal of Pharmacology</i> , <b>2008</b> , 584, 376-89   | 5.3  | 9  |
| 25 | Proposition of a feasible protocol to evaluate salt sensitivity in a population-based setting. <i>Hypertension Research</i> , <b>2002</b> , 25, 801-9  | 4.7  | 8  |
| 24 | Investigation of Functional Genes at Homologous Loci Identified Based on Genome-wide Association Studies of Blood Lipids via High-fat Diet Intervention in Rats using an in vivo Approach. <i>Journal of Atherosclerosis and Thrombosis</i> , <b>2015</b> , 22, 455-80 | 4    | 7  |
| 23 | Systematic fine-mapping of association with BMI and type 2 diabetes at the FTO locus by integrating results from multiple ethnic groups. <i>PLoS ONE</i> , <b>2014</b> , 9, e101329  | 3.7  | 7  |
| 22 | Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , <b>2022</b> ,   | 36.3 | 7  |
| 21 | Disease-associated polymorphisms in 9p21 are not associated with extreme longevity. <i>Geriatrics and Gerontology International</i> , <b>2015</b> , 15, 797-803  | 2.9  | 6  |
| 20 | LOX-1 (Lectin-Like Oxidized Low-Density Lipoprotein Receptor-1) Deletion Has Protective Effects on Stroke in the Genetic Background of Stroke-Prone Spontaneously Hypertensive Rat. <i>Stroke</i> , <b>2020</b> , 51, 1835-1843  | 6.7  | 6  |
| 19 | HapMap coverage for SNPs in the Japanese population. <i>Journal of Human Genetics</i> , <b>2008</b> , 53, 96-99  | 4.3  | 6  |
| 18 | Evaluation of insulin resistance linkage to rat chromosome 4 in SHR of a Japanese colony. <i>Biochemical and Biophysical Research Communications</i> , <b>2005</b> , 329, 879-87   | 3.4  | 6  |
| 17 | Alterations of lipid metabolism, blood pressure and fatty liver in spontaneously hypertensive rats transgenic for human cholesteryl ester transfer protein. <i>Hypertension Research</i> , <b>2020</b> , 43, 655-666   | 4.7  | 4  |
| 16 | Ethnic diversity in type 2 diabetes genetics between East Asians and Europeans. <i>Journal of Diabetes Investigation</i> , <b>2012</b> , 3, 349-51   | 3.9  | 4  |
| 15 | Identification of type 2 diabetes loci in 433,540 East Asian individuals   |      | 4  |

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|----|---|------|---|
| 14 | Further dissection of QTLs for salt-induced stroke and identification of candidate genes in the stroke-prone spontaneously hypertensive rat. <i>Scientific Reports</i> , <b>2018</b> , 8, 9403  | 4.9  | 4 |
| 13 | SLC15A4 mediates M1-prone metabolic shifts in macrophages and guards immune cells from metabolic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,  | 11.5 | 4 |
| 12 | Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2111-2125  | 15.1 | 3 |
| 11 | Candesartan-induced gene expression in five organs of stroke-prone spontaneously hypertensive rats. <i>Hypertension Research</i> , <b>2008</b> , 31, 1963-75  | 4.7  | 3 |
| 10 | Dynamic changes of the renin-angiotensin and associated systems in the rat after pharmacological and dietary interventions in vivo. <i>Physiological Genomics</i> , <b>2008</b> , 35, 330-40  | 3.6  | 3 |
| 9  | Nonlinear ridge regression improves cell-type-specific differential expression analysis. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 141  | 3.6  | 3 |
| 8  | A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study.. <i>European Heart Journal</i> , <b>2022</b> ,  | 9.5  | 3 |
| 7  | Heterogeneous effects of association between blood pressure loci and coronary artery disease in east Asian individuals. <i>Circulation Journal</i> , <b>2015</b> , 79, 830-8  | 2.9  | 2 |
| 6  | Transcriptomic Response in the Heart and Kidney to Different Types of Antihypertensive Drug Administration. <i>Hypertension</i> , <b>2021</b> , HYPERTENSIONAHA12118026   | 8.5  | 2 |
| 5  | Integrative genomic analysis of blood pressure and related phenotypes in rats. <i>DMM Disease Models and Mechanisms</i> , <b>2021</b> , 14,   | 4.1  | 2 |
| 4  | Effects of maternal and fetal choline concentrations on the fetal growth and placental DNA methylation of 12 target genes related to fetal growth, adipogenesis, and energy metabolism. <i>Journal of Obstetrics and Gynaecology Research</i> , <b>2021</b> , 47, 734-744 | 1.9  | 2 |
| 3  | Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. <i>Communications Biology</i> , <b>2022</b> , 5, 329   | 6.7  | 2 |
| 2  | Candidate genes revisited in the genetics of hypertension and blood pressure. <i>Hypertension Research</i> , <b>2013</b> , 36, 1032-4   | 4.7  | 1 |
| 1  | Venous thromboembolism is caused by prothrombin p.Arg541Trp mutation in Japanese individuals. <i>Human Genome Variation</i> , <b>2021</b> , 8, 13   | 1.8  | 1 |